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Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=6; day=29; hr=11; min=20; sec=18; ms=38; ]

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Application No: 10538201

Version No: 3.0

Input Set:

Output Set:

Started: 2010-06-18 18:44:41.288

Finished: 2010-06-18 18:44:43.942

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 654 ms

Total Warnings: 15

Total Errors: 0

No. of SeqIDs Defined: 48

Actual SeqID Count: 48

Error code	Error Description
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# SEQUENCE LISTING

<110> Novartis AG

<120> ANTIBODY (11C7) ANTI NOGO A AND ITS PHARMACEUTICAL USE

<130> 4-32761P1/UNZ

<140> 10538201

<141> 2006-03-08

<150> PCT/EP03/13960

<151> 2003-12-09

<150> UK 0228832.2

<151> 2002-10-12

<160> 48

<170> PatentIn version 3.5

<210> 1

<211> 18

<212> PRT

<213> Rattus norvegicus

<220>

<221> PEPTIDE

<222> (1)..(18)

<223> rat NogoA\_623-640

<400> 1

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Glu Ala

<210> 2

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<212> PRT

<213> Mus musculus

<220>

<221> CHAIN

<222> (1)..(221)

<223> Variable part of Heavy Chain of 11C7 with leader sequence

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Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg	35	40	45
Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu	50	55	60
Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro	65	70	75
Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr	85	90	95
Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr	100	105	110
Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln	115	120	125
Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val	130	135	140
Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr	145	150	155
Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr	165	170	175
Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val	180	185	190
Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser	195	200	205
Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala	210	215	220

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<211> 238

<212> PRT  
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<220>  
<221> CHAIN  
<222> (1)..(238)  
<223> Light Chain of 11C7 with leader sequence

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20 25 30

Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu  
35 40 45

Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro  
50 55 60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser  
65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr  
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys  
100 105 110

Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu  
115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro  
130 135 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu  
145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly  
165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser  
180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp  
 195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr  
 210 215 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

<210> 4  
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 <212> DNA  
 <213> Homo sapiens

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 <221> CDS  
 <222> (1)..(3579)  
 <223> Human NogoA

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 ccc cgg ccg cag ccc gcg ttc aag tac cag ttc gtg agg gag ccc gag 96  
 Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu  
 20 25 30  
 gac gag gag gaa gaa gag gag gag gaa gag gag gac gag gac gaa gac 144  
 Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp  
 35 40 45  
 ctg gag gag ctg gag gtg ctg gag agg aag ccc gcc gcc ggg ctg tcc 192  
 Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser  
 50 55 60  
 gcg gcc cca gtg ccc acc gcc cct gcc gcc ggc gcg ccc ctg atg gac 240  
 Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp  
 65 70 75 80  
 ttc gga aat gac ttc gtg ccg ccg gcg ccc cgg gga ccc ctg ccg gcc 288  
 Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala  
 85 90 95  
 gct ccc ccc gtc gcc ccg gag ccg cag ccg tct tgg gac ccg agc ccg 336  
 Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro  
 100 105 110  
 gtg tcg tcg acc gtg ccc gcg cca tcc ccg ctg tct gct gcc gca gtc 384  
 Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val  
 115 120 125

tcg ccc tcc aag ctc cct gag gac gac gag cct ccg gcc cgg cct ccc	432
Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro	
130 135 140	
cct cct ccc ccg gcc agc gtg agc ccc cag gca gag ccc gtg tgg acc	480
Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr	
145 150 155 160	
ccg cca gcc ccg gct ccc gcc gcg ccc ccc tcc acc ccg gcc gcg ccc	528
Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro	
165 170 175	
aag cgc agg ggc tcc tcg ggc tca gtg gat gag acc ctt ttt gct ctt	576
Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu	
180 185 190	
cct gct gca tct gag cct gtg ata cgc tcc tct gca gaa aat atg gac	624
Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp	
195 200 205	
ttg aag gag cag cca ggt aac act att tcg gct ggt caa gag gat ttc	672
Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe	
210 215 220	
cca tct gtc ctg ctt gaa act gct gct tct ctt cct tct ctg tct cct	720
Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro	
225 230 235 240	
ctc tca gcc gct tct ttc aaa gaa cat gaa tac ctt ggt aat ttg tca	768
Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser	
245 250 255	
aca gta tta ccc act gaa gga aca ctt caa gaa aat gtc agt gaa gct	816
Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala	
260 265 270	
tct aaa gag gtc tca gag aag gca aaa act cta ctc ata gat aga gat	864
Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp	
275 280 285	
tta aca gag ttt tca gaa tta gaa tac tca gaa atg gga tca tcg ttc	912
Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe	
290 295 300	
agt gtc tct cca aaa gca gaa tct gcc gta ata gta gca aat cct agg	960
Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg	
305 310 315 320	
gaa gaa ata atc gtg aaa aat aaa gat gaa gaa gag aag tta gtt agt	1008
Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser	
325 330 335	
aat aac atc ctt cat aat caa caa gag tta cct aca gct ctt act aaa	1056
Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys	
340 345 350	

ttg gtt aaa gag gat gaa gtt gtg tct tca gaa aaa gca aaa gac agt	1104
Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser	
355 360 365	
ttt aat gaa aag aga gtt gca gtg gaa gct cct atg agg gag gaa tat	1152
Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr	
370 375 380	
gca gac ttc aaa cca ttt gag cga gta tgg gaa gtg aaa gat agt aag	1200
Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys	
385 390 395 400	
gaa gat agt gat atg ttg gct gct gga ggt aaa atc gag agc aac ttg	1248
Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu	
405 410 415	
gaa agt aaa gtg gat aaa aaa tgt ttt gca gat agc ctt gag caa act	1296
Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr	
420 425 430	
aat cac gaa aaa gat agt gag agt agt aat gat gat act tct ttc ccc	1344
Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro	
435 440 445	
agt acg cca gaa ggt ata aag gat cgt tca gga gca tat atc aca tgt	1392
Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys	
450 455 460	
gct ccc ttt aac cca gca gca act gag agc att gca aca aac att ttt	1440
Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe	
465 470 475 480	
cct ttg tta gga gat cct act tca gaa aat aag acc gat gaa aaa aaa	1488
Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys	
485 490 495	
ata gaa gaa aag aag gcc caa ata gta aca gag aag aat act agc acc	1536
Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr	
500 505 510	
aaa aca tca aac cct ttt ctt gta gca gca cag gat tct gag aca gat	1584
Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp	
515 520 525	
tat gtc aca aca gat aat tta aca aag gtg act gag gaa gtc gtg gca	1632
Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala	
530 535 540	
aac atg cct gaa ggc ctg act cca gat tta gta cag gaa gca tgt gaa	1680
Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu	
545 550 555 560	
agt gaa ttg aat gaa gtt act ggt aca aag att gct tat gaa aca aaa	1728
Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys	
565 570 575	
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Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro	
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Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser	
595 600 605	
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Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val	
610 615 620	
cct agt gct ggt gct tcc gtg ata cag ccc agc tca tca cca tta gaa	1920
Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu	
625 630 635 640	
gct tct tca gtt aat tat gaa agc ata aaa cat gag cct gaa aac ccc	1968
Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro	
645 650 655	
cca cca tat gaa gag gcc atg agt gta tca cta aaa aaa gta tca gga	2016
Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly	
660 665 670	
ata aag gaa gaa att aaa gag cct gaa aat att aat gca gct ctt caa	2064
Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln	
675 680 685	
gaa aca gaa gct cct tat ata tct att gca tgt gat tta att aaa gaa	2112
Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu	
690 695 700	
aca aag ctt tct gct gaa cca gct ccg gat ttc tct gat tat tca gaa	2160
Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu	
705 710 715 720	
atg gca aaa gtt gaa cag cca gtg cct gat cat tct gag cta gtt gaa	2208
Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu	
725 730 735	
gat tcc tca cct gat tct gaa cca gtt gac tta ttt agt gat gat tca	2256
Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser	
740 745 750	
ata cct gac gtt cca caa aaa caa gat gaa act gtg atg ctt gtg aaa	2304
Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys	
755 760 765	
gaa agt ctc act gag act tca ttt gag tca atg ata gaa tat gaa aat	2352
Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn	
770 775 780	
aag gaa aaa ctc agt gct ttg cca cct gag gga gga aag cca tat ttg	2400
Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu	
785 790 795 800	
gaa tct ttt aag ctc agt tta gat aac aca aaa gat acc ctg tta cct	2448
Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro	

805	810	815	
gat gaa gtt tca aca ttg agc aaa aag gag aaa att cct ttg cag atg			2496
Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met			
820	825	830	
gag gag ctc agt act gca gtt tat tca aat gat gac tta ttt att tct			2544
Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser			
835	840	845	
aag gaa gca cag ata aga gaa act gaa acg ttt tca gat tca tct cca			2592
Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro			
850	855	860	
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Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp			
865	870	875	880
tca ttt tct aaa tta gcc agg gaa tat act gac cta gaa gta tcc cac			2688
Se			